

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
INTERFERON
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Foley & Lardner
(B) STREET: 3000 K Street, N.W., Suite 500
(C) CITY: Washington
(D) STATE: D.C.
(E) ZIP: 20007
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/307,588
(B) FILING DATE: 05-DEC-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP93/00770
(B) FILING DATE: 30-MAR-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 92400902.0
(B) FILING DATE: 31-MAR-1992
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SAXE, Bernhard D.
(B) REGISTRATION NUMBER: 28,665
(C) REFERENCE/DOCKET NUMBER: 17283/117/GUPL
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202)672-5300
(B) TELEFAX: (202)672-5399

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1334

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGCAGGGAT CTGCGGCGGC TCOCAG	ATG	ATG	GTC	GTC	CTC	CTG	GGC	GCG	ACG		53
	Met	Met	Val	Val	Leu	Leu	Gly	Ala	Thr		
	1				5						
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA											101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala											
10				15				20		25	
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA											149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile				30			35			40	
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG											197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly				45			50			55	
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG											245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp				60			65			70	
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT											293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe				75			80			85	
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA											341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg				90		95				100	105
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA											389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr				110			115			120	
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT											437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala				125			130			135	
GAA GAT AAG GCA ATA GTG ATA CAC ATC TCT CCT GGA ACA AAA GAT AGT											485
Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly Thr Lys Asp Ser				140			145			150	
GTT ATG TGG GCT TTG GAT GGT TTA AGC TTT ACA TAT AGC TTA CTT ATC											533
Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr Tyr Ser Leu Leu Ile				155			160			165	
TGG AAA AAC TCT TCA GGT GTA GAA GAA AGG ATT GAA AAT ATT TAT TCC											581
Trp Lys Asn Ser Ser Gly Val Glu Glu Arg Ile Glu Asn Ile Tyr Ser				170		175			180		185
AGA CAT AAA ATT TAT AAA CTC TCA CCA GAG ACT ACT TAT TGT CTA AAA											629
Arg His Lys Ile Tyr Lys Leu Ser Pro Glu Thr Thr Tyr Cys Leu Lys				190			195			200	
GTT AAA GCA GCA CTA CTT ACG TCA TGG AAA ATT GGT GTC TAT AGT CCA											677
Val Lys Ala Ala Leu Leu Thr Ser Trp Lys Ile Gly Val Tyr Ser Pro				205			210			215	
GTA CAT TGT ATA AAG ACC ACA GTT GAA AAT GAA CTA CCT CCA CCA GAA											725
Val His Cys Ile Lys Thr Thr Val Glu Asn Glu Leu Pro Pro Pro Glu				220			225			230	
AAT ATA GAA GTC AGT GTC CAA AAT CAG AAC TAT GTT CTT AAA TGG GAT											773
Asn Ile Glu Val Ser Val Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp				235		240			245		

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TAT	ACA	TAT	GCA	AAC	ATG	ACC	TTT	CAA	GTT	CAG	TGG	CTC	CAC	GCC	TTT	821
Tyr	Thr	Tyr	Ala	Asn	Met	Thr	Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	
250					255					260					265	
TTA	AAA	AGG	AAT	CCT	GGA	AAC	CAT	TTG	TAT	AAA	TGG	AAA	CAA	ATA	CCT	869
Leu	Lys	Arg	Asn	Pro	Gly	Asn	His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	
				270				275							280	
GAC	TGT	GAA	AAT	GTC	AAA	ACT	ACC	CAG	TGT	GTC	TTT	CCT	CAA	AAC	GTT	917
Asp	Cys	Glu	Asn	Val	Lys	Thr	Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	
			285					290					295			
TTC	CAA	AAA	GGA	ATT	TAC	CTT	CTC	CGC	GTA	CAA	GCA	TCT	GAT	GGA	AAT	965
Phe	Gln	Lys	Gly	Ile	Tyr	Leu	Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	
		300					305					310				
AAC	ACA	TCT	TTT	TGG	TCT	GAA	GAG	ATA	AAG	TTT	GAT	ACT	GAA	ATA	CAA	1013
Asn	Thr	Ser	Phe	Trp	Ser	Glu	Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	
		315				320					325					
GCT	TTC	CTA	CTT	CCT	CCA	GTC	TTT	AAC	ATT	AGA	TCC	CTT	AGT	GAT	TCA	1061
Ala	Phe	Leu	Leu	Pro	Pro	Val	Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	
					335					340					345	
TTC	CAT	ATC	TAT	ATC	GGT	GCT	CCA	AAA	CAG	TCT	GGA	AAC	ACG	CCT	GTG	1109
Phe	His	Ile	Tyr	Ile	Gly	Ala	Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	
				350					355					360		
ATC	CAG	GAT	TAT	CCA	CTG	ATT	TAT	GAA	ATT	ATT	TTT	TGG	GAA	AAC	ACT	1157
Ile	Gln	Asp	Tyr	Pro	Leu	Ile	Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	
			365					370					375			
TCA	AAT	GCT	GAG	AGA	AAA	ATT	ATC	GAG	AAA	AAA	ACT	GAT	GTT	ACA	GTT	1205
Ser	Asn	Ala	Glu	Arg	Lys	Ile	Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	
		380					385					390				
CCT	AAT	TTG	AAA	CCA	CTG	ACT	GTA	TAT	TGT	GTG	AAA	GCC	AGA	GCA	CAC	1253
Pro	Asn	Leu	Lys	Pro	Leu	Thr	Val	Tyr	Cys	Val	Lys	Ala	Arg	Ala	His	
		395				400					405					
ACC	ATG	GAT	GAA	AAG	CTG	AAT	AAA	AGC	AGT	GTT	TTT	AGT	GAC	GCT	GTA	1301
Thr	Met	Asp	Glu	Lys	Leu	Asn	Lys	Ser	Ser	Val	Phe	Ser	Asp	Ala	Val	
					415					420					425	
TGT	GAG	AAA	ACA	AAA	CCA	GGA	AAT	ACC	TCT	AAA	TGAGGTACC					1343
Cys	Glu	Lys	Thr	Lys	Pro	Gly	Asn	Thr	Ser	Lys						
				430					435							

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Met	Val	Val	Leu	Leu	Gly	Ala	Thr	Thr	Leu	Val	Leu	Val	Ala	Val	
1				5					10					15		
Gly	Pro	Trp	Val	Leu	Ser	Ala	Ala	Ala	Gly	Gly	Lys	Asn	Leu	Lys	Ser	
			20				25						30			

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
50 55 60

Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile Lys Leu Ser Gly Cys Gln
65 70 75 80

Asn Ile Thr Ser Thr Lys Cys Asn Phe Ser Ser Leu Lys Leu Asn Val
85 90 95

Tyr Glu Glu Ile Lys Leu Arg Ile Arg Ala Glu Lys Glu Asn Thr Ser
100 105 110

Ser Trp Tyr Glu Val Asp Ser Phe Thr Pro Phe Arg Lys Ala Gln Ile
115 120 125

Gly Pro Pro Glu Val His Leu Glu Ala Glu Asp Lys Ala Ile Val Ile
130 135 140

His Ile Ser Pro Gly Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly
145 150 155 160

Leu Ser Phe Thr Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val
165 170 175

Glu Glu Arg Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu
180 185 190

Ser Pro Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr
195 200 205

Ser Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr
210 215 220

Val Glu Asn Glu Leu Pro Pro Glu Asn Ile Glu Val Ser Val Gln
225 230 235 240

Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn Met Thr
245 250 255

Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn Pro Gly Asn
260 265 270

His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu Asn Val Lys Thr
275 280 285

Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln Lys Gly Ile Tyr Leu
290 295 300

Leu Arg Val Gln Ala Ser Asp Gly Asn Asn Thr Ser Phe Trp Ser Glu
305 310 315 320

Glu Ile Lys Phe Asp Thr Glu Ile Gln Ala Phe Leu Leu Pro Pro Val
325 330 335

Phe Asn Ile Arg Ser Leu Ser Asp Ser Phe His Ile Tyr Ile Gly Ala
340 345 350

Pro Lys Gln Ser Gly Asn Thr Pro Val Ile Gln Asp Tyr Pro Leu Ile
355 360 365

Tyr Glu Ile Ile Phe Trp Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile
370 375 380

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Ile Glu Lys Lys Thr Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr
385 390 395 400
Val Tyr Cys Val Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn
405 410 415
Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430
Asn Thr Ser Lys
435

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1755 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTGCAGGGAT CTGCGGCGGC TCCCAG ATG ATG GTC GTC CTC CTG GGC GCG ACG	53
Met Met Val Val Leu Leu Gly Ala Thr	
1 5	
ACC CTA GTG CTC GTC GCC GTG GGC CCA TGG GTG TTG TCC GCA GCC GCA	101
Thr Leu Val Leu Val Ala Val Gly Pro Trp Val Leu Ser Ala Ala Ala	
10 15 20 25	
GGT GGA AAA AAT CTA AAA TCT CCT CAA AAA GTA GAG GTC GAC ATC ATA	149
Gly Gly Lys Asn Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile	
30 35 40	
GAT GAC AAC TTT ATC CTG AGG TGG AAC AGG AGC GAT GAG TCT GTC GGG	197
Asp Asp Asn Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly	
45 50 55	
AAT GTG ACT TTT TCA TTC GAT TAT CAA AAA ACT GGG ATG GAT AAT TGG	245
Asn Val Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp	
60 65 70	
ATA AAA TTG TCT GGG TGT CAG AAT ATT ACT AGT ACC AAA TGC AAC TTT	293
Ile Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe	
75 80 85	
TCT TCA CTC AAG CTG AAT GTT TAT GAA GAA ATT AAA TTG CGT ATA AGA	341
Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile Arg	
90 95 100 105	
GCA GAA AAA GAA AAC ACT TCT TCA TGG TAT GAG GTT GAC TCA TTT ACA	389
Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser Phe Thr	
110 115 120	
CCA TTT CGC AAA GCT CAG ATT GGT CCT CCA GAA GTA CAT TTA GAA GCT	437
Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His Leu Glu Ala	
125 130 135	

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GAA Glu	GAT Asp	AAG Lys 140	GCA Ala	ATA Ile	GTG Val	ATA Ile	CAC His 145	ATC Ile	TCT Ser	CCT Pro	GGA Gly 150	ACA Thr 150	AAA Lys	GAT Asp	AGT Ser	485
GTT Val 155	ATG Met	TGG Trp	GCT Ala	TTG Leu	GAT Asp 160	GGT Gly 160	TTA Leu	AGC Ser	TTT Phe	ACA Thr	TAT Tyr 165	AGC Ser	TTA Leu	CTT Leu	ATC Ile	533
TGG Trp 170	AAA Lys	AAC Asn	TCT Ser	TCA Ser	GGT Gly 175	GTA Val	GAA Glu	GAA Glu	AGG Arg	ATT Ile 180	GAA Glu	AAT Asn	ATT Ile	TAT Tyr	TCC Ser 185	581
AGA Arg	CAT His	AAA Lys	ATT Ile	TAT Tyr 190	AAA Lys	CTC Leu	TCA Ser	CCA Pro	GAG Glu 195	ACT Thr	ACT Thr	TAT Tyr	TGT Cys	CTA Leu 200	AAA Lys	629
GTT Val	AAA Lys	GCA Ala	GCA Ala 205	CTA Leu	CTT Leu	ACG Thr	TCA Ser	TGG Trp 210	AAA Lys	ATT Ile	GGT Gly	GTC Val	TAT Tyr 215	AGT Ser	CCA Pro	677
GTA Val	CAT His	TGT Cys 220	ATA Ile	AAG Lys	ACC Thr	ACA Thr 225	GTT Val	GAA Glu	AAT Asn	GAA Glu	CTA Leu	CCT Pro 230	CCA Pro	CCA Pro	GAA Glu	725
AAT Asn 235	ATA Ile	GAA Glu	GTC Val	AGT Ser	GTC Val	CAA Gln 240	AAT Asn	CAG Gln	AAC Asn	TAT Tyr	GTT Val 245	CTT Leu	AAA Lys	TGG Trp	GAT Asp	773
TAT Tyr 250	ACA Thr	TAT Tyr	GCA Ala	AAC Asn	ATG Met 255	ACC Thr	TTT Phe	CAA Gln	GTT Val	CAG Gln	TGG Trp 260	CTC Leu	CAC His	GCC Ala	TTT Phe 265	821
TTA Leu	AAA Lys	AGG Arg	AAT Asn	CCT Pro 270	GGA Gly	AAC Asn	CAT His	TTG Leu 275	TAT Tyr	AAA Lys	TGG Trp	AAA Lys	CAA Gln	ATA Ile 280	CCT Pro	869
GAC Asp	TGT Cys	GAA Glu 285	AAT Asn	GTC Val	AAA Lys	ACT Thr	ACC Thr	CAG Gln 290	TGT Cys	GTC Val	TTT Phe	CCT Pro	CAA Gln 295	AAC Asn	GTT Val	917
TTC Phe	CAA Gln 300	AAA Lys	GGA Gly	ATT Ile	TAC Tyr	CTT Leu	CTC Leu 305	CGC Arg	GTA Val	CAA Gln	GCA Ala	TCT Ser 310	GAT Asp	GGA Gly	AAT Asn	965
AAC Asn 315	ACA Thr	TCT Ser	TTT Phe	TGG Trp	TCT Ser	GAA Glu 320	GAG Glu	ATA Ile	AAG Lys	TTT Phe	GAT Asp 325	ACT Thr	GAA Glu	ATA Ile	CAA Gln	1013
GCT Ala 330	TTC Phe	CTA Leu	CTT Leu	CCT Pro	CCA Pro 335	GTC Val	TTT Phe	AAC Asn	ATT Ile	AGA Arg 340	TCC Ser	CTT Leu	AGT Ser	GAT Asp	TCA Ser 345	1061
TTC Phe	CAT His	ATC Ile	TAT Tyr	ATC Ile 350	GGT Gly	GCT Ala	CCA Pro	AAA Lys	CAG Gln 355	TCT Ser	GGA Gly	AAC Asn	ACG Thr	CCT Pro	GTG Val 360	1109
ATC Ile	CAG Gln	GAT Asp	TAT Tyr 365	CCA Pro	CTG Leu	ATT Ile	TAT Tyr	GAA Glu 370	ATT Ile	ATT Ile	TTT Phe	TGG Trp	GAA Glu	AAC Asn	ACT Thr	1157
TCA Ser	AAT Asn 380	GCT Ala	GAG Glu	AGA Arg	AAA Lys	ATT Ile	ATC Ile 385	GAG Glu	AAA Lys	AAA Lys	ACT Thr	GAT Asp 390	GTT Val	ACA Thr	GTT Val	1205
CCT Pro 395	AAT Asn	TTG Leu	AAA Lys	CCA Pro	CTG Leu	ACT Thr 400	GTA Val	TAT Tyr	TGT Cys	GTG Val	AAA Ala 405	GCC Ala	AGA Arg	GCA Ala	CAC His	1253

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ACC ATG GAT GAA AAG CTG AAT AAA AGC AGT GTT TTT AGT GAC GCT GTA 1301
 Thr Met Asp Glu Lys Leu Asn Lys Ser Ser Val Phe Ser Asp Ala Val
 410 415 420 425

TGT GAG AAA ACA AAA CCA GGA AAT ACC TCT AAA ATT TGG CTT ATA GTT 1349
 Cys Glu Lys Thr Lys Pro Gly Asn Thr Ser Lys Ile Trp Leu Ile Val
 430 435 440

GGA ATT TGT ATT GCA TTA TTT GCT CTC CCG TTT GTC ATT TAT GCT GCG 1397
 Gly Ile Cys Ile Ala Leu Phe Ala Leu Pro Phe Val Ile Tyr Ala Ala
 445 450 455

AAA GTC TTC TTG AGA TGC ATC AAT TAT GTC TTC TTT CCA TCA CTT AAA 1445
 Lys Val Phe Leu Arg Cys Ile Asn Tyr Val Phe Phe Pro Ser Leu Lys
 460 465 470

CCT TCT TCC AGT ATA GAT GAG TAT TTC TCT GAA CAG CCA TTG AAG AAT 1493
 Pro Ser Ser Ser Ile Asp Glu Tyr Phe Ser Glu Gln Pro Leu Lys Asn
 475 480 485

CTT CTG CTT TCA ACT TCT GAG GAA CAA ATC GAA AAA TGT TTC ATA ATT 1541
 Leu Leu Leu Ser Thr Ser Glu Glu Gln Ile Glu Lys Cys Phe Ile Ile
 490 495 500 505

GAA AAT ATA AGC ACA ATT GCT ACA GTA GAA GAA ACT AAT CAA ACT GAT 1589
 Glu Asn Ile Ser Thr Ile Ala Thr Val Glu Glu Thr Asn Gln Thr Asp
 510 515 520

GAA GAT CAT AAA AAA TAC AGT TCC CAA ACT AGC CAA GAT TCA GGA AAT 1637
 Glu Asp His Lys Lys Tyr Ser Ser Gln Thr Ser Gln Asp Ser Gly Asn
 525 530 535

TAT TCT AAT GAA GAT GAA AGC GAA AGT AAA ACA AGT GAA GAA CTA CAG 1685
 Tyr Ser Asn Glu Asp Glu Ser Glu Ser Lys Thr Ser Glu Glu Leu Gln
 540 545 550

CAG GAC TTT GTA TGACCAGAAA TGAAGTGTGT CAAGTATAAG GTTTTTTCAGC 1737
 Gln Asp Phe Val
 555

AGGAGTTACA CTGGTACC 1755

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 557 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Met Val Val Leu Leu Gly Ala Thr Thr Leu Val Leu Val Ala Val
 1 5 10 15

Gly Pro Trp Val Leu Ser Ala Ala Ala Gly Gly Lys Asn Leu Lys Ser
 20 25 30

Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn Phe Ile Leu Arg
 35 40 45

Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val Thr Phe Ser Phe Asp
 50 55 60

Tyr	Gln	Lys	Thr	Gly	Met	Asp	Asn	Trp	Ile	Lys	Leu	Ser	Gly	Cys	Gln	
65					70					75					80	
Asn	Ile	Thr	Ser	Thr	Lys	Cys	Asn	Phe	Ser	Ser	Leu	Lys	Leu	Asn	Val	
				85					90					95		
Tyr	Glu	Glu	Ile	Lys	Leu	Arg	Ile	Arg	Ala	Glu	Lys	Glu	Asn	Thr	Ser	
			100					105					110			
Ser	Trp	Tyr	Glu	Val	Asp	Ser	Phe	Thr	Pro	Phe	Arg	Lys	Ala	Gln	Ile	
		115					120					125				
Gly	Pro	Pro	Glu	Val	His	Leu	Glu	Ala	Glu	Asp	Lys	Ala	Ile	Val	Ile	
	130					135					140					
His	Ile	Ser	Pro	Gly	Thr	Lys	Asp	Ser	Val	Met	Trp	Ala	Leu	Asp	Gly	
145					150					155					160	
Leu	Ser	Phe	Thr	Tyr	Ser	Leu	Leu	Ile	Trp	Lys	Asn	Ser	Ser	Gly	Val	
				165					170					175		
Glu	Glu	Arg	Ile	Glu	Asn	Ile	Tyr	Ser	Arg	His	Lys	Ile	Tyr	Lys	Leu	
			180					185					190			
Ser	Pro	Glu	Thr	Thr	Tyr	Cys	Leu	Lys	Val	Lys	Ala	Ala	Leu	Leu	Thr	
		195					200					205				
Ser	Trp	Lys	Ile	Gly	Val	Tyr	Ser	Pro	Val	His	Cys	Ile	Lys	Thr	Thr	
	210					215					220					
Val	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Glu	Asn	Ile	Glu	Val	Ser	Val	Gln	
225					230					235					240	
Asn	Gln	Asn	Tyr	Val	Leu	Lys	Trp	Asp	Tyr	Thr	Tyr	Ala	Asn	Met	Thr	
				245					250					255		
Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	Leu	Lys	Arg	Asn	Pro	Gly	Asn	
			260					265					270			
His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	Asp	Cys	Glu	Asn	Val	Lys	Thr	
	275						280					285				
Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	Phe	Gln	Lys	Gly	Ile	Tyr	Leu	
	290					295					300					
Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	Asn	Thr	Ser	Phe	Trp	Ser	Glu	
305					310					315					320	
Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	Ala	Phe	Leu	Leu	Pro	Pro	Val	
				325					330					335		
Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	Ser	Phe	His	Ile	Tyr	Ile	Gly	Ala	
			340					345					350			
Pro	Lys	Gln	Ser	Gly	Asn	Thr	Pro	Val	Ile	Gln	Asp	Tyr	Pro	Leu	Ile	
		355					360					365				
Tyr	Glu	Ile	Ile	Phe	Trp	Glu	Asn	Thr	Ser	Asn	Ala	Glu	Arg	Lys	Ile	
	370					375					380					
Ile	Glu	Lys	Lys	Thr	Asp	Val	Thr	Val	Pro	Asn	Leu	Lys	Pro	Leu	Thr	
385					390					395				400		
Val	Tyr	Cys	Val	Lys	Ala	Arg	Ala	His	Thr	Met	Asp	Glu	Lys	Leu	Asn	
				405					410					415		

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Sub 1

Lys Ser Ser Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly
420 425 430
Asn Thr Ser Lys Ile Trp Leu Ile Val Gly Ile Cys Ile Ala Leu Phe
435 440 445
Ala Leu Pro Phe Val Ile Tyr Ala Ala Lys Val Phe Leu Arg Cys Ile
450 455 460
Asn Tyr Val Phe Phe Pro Ser Leu Lys Pro Ser Ser Ser Ile Asp Glu
465 470 475 480
Tyr Phe Ser Glu Gln Pro Leu Lys Asn Leu Leu Leu Ser Thr Ser Glu
485 490 495
Glu Gln Ile Glu Lys Cys Phe Ile Ile Glu Asn Ile Ser Thr Ile Ala
500 505 510
Thr Val Glu Glu Thr Asn Gln Thr Asp Glu Asp His Lys Lys Tyr Ser
515 520 525
Ser Gln Thr Ser Gln Asp Ser Gly Asn Tyr Ser Asn Glu Asp Glu Ser
530 535 540
Glu Ser Lys Thr Ser Glu Glu Leu Gln Gln Asp Phe Val
545 550 555

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WRITEENABLE
WRITEPROTECT



IBM PC AT 1.44mb MSDOS 3.3

~~BENOIT, et al.~~

~~US 08/307,588~~

~~FILED:05-DEC-1994~~

~~"MONOCLONAL ANTIBODIES~~

~~AGAINST THE INTERFERON..."~~

~~ATTY DOCKET:17283/117/GUPL~~

~~DATA REC'D:26 MAR 1996~~